RAW SEQUENCE LISTING
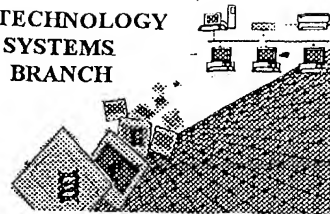# ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *10/675,226*

Source: *IFWO -01PL*

Date Processed by STIC: *10/7/2003*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
         http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/2003):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/2003

IFWO

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RAW SEQUENCE LISTING                         DATE: 10/07/2003
PATENT APPLICATION:  US/10/675,226           TIME: 14:16:37

            Input Set : A:\14233.10USU1-Romeo-Sequence Listing.txt
            Output Set: N:\CRF4\10072003\J675226.raw

                    SEQUENCE LISTING
        4  (1) GENERAL INFORMATION:
C-->    7        (i)  APPLICANT: Romeo, Tony
W-->   25       (ii)  TITLE OF INVENTION: Methods for Polysaccharide Adhesin Synthesis
       26                               Modulation
       28      (iii)  NUMBER OF SEQUENCES: 9
W-->   17            (B)  STREET: c/o Ridout & Maybee
       18            (C)  CITY: Toronto
       19            (D)  STATE: Ont
       20            (E)  COUNTRY: Canada
C-->   21            (F)  ZIP: M5C 3B1
C-->   30        (v)  COMPUTER READABLE FORM:
       31            (A)  MEDIUM TYPE: Floppy disk
       32            (B)  COMPUTER: IBM PC compatible
       33            (C)  OPERATING SYSTEM: PC-DOS/MS-DOS
       34            (D)  SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
C-->   36       (vi)  CURRENT APPLICATION DATA:
C-->   37            (A)  APPLICATION NUMBER: US/10/675,226
C-->    0            (B)  FILING DATE: 29-Sep-2003
C-->    0     (viii)  ATTORNEY/AGENT INFORMATION:
W-->   16            (A)  NAME: Wang, Xin
C-->    0       (ix)  TELECOMMUNICATION INFORMATION:
C-->   22            (A)  TELEPHONE: 4168653505
C-->   23            (B)  TELEFAX: 4163621482
       39  (2) INFORMATION FOR SEQ ID NO: 1:
       41        (i)  SEQUENCE CHARACTERISTICS:
       42            (A)  LENGTH: 2460 base pairs
       43            (B)  TYPE: nucleic acid
       44            (C)  STRANDEDNESS: unknown
       45            (D)  TOPOLOGY: unknown
       47       (ii)  MOLECULE TYPE: DNA (genomic)
       49      (iii)  HYPOTHETICAL: NO
C-->   51       (iv)  ANTI-SENSE: NO
       53       (vi)  ORIGINAL SOURCE:
       54            (A)  ORGANISM: E. coli
       57      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 1:
       59 ATGTATTCAA GTAGCAGAAA AAGGTGCCCG AAAACCAAAT GGGCTTTGAA ACTTCTTACT        60
       61 GCCGCATTTT TAGCAGCGAG TCCCGCGGCG AAGAGTGCTG TTAATAACGC CTATGATGCA       120
       63 TTGATTATTG AAGCTCGCAA GGGTAATACT CAGCCAGCTT TGTCATGGTT TGCACTAAAA       180
       65 TCAGCACTCA GCAATAACCA AATTGCTGAC TGGTTACAGA TTGCCTTATG GGCCGGGCAA       240
       67 GATAAACAGG TTATTACCGT TTACAACCGC TACCGTCATC AGCAATTACC AGCGCGTGGT       300
       69 TATGCAGCTG TCGCCGTCGC TTATCGTAAC CTGCAACAAT GGCAAAACTC GCTTACACTG       360
       71 TGGCAAAAGG CGCTCTCTCT GGAGCCGCAA AATAAGGATT ATCAACGGGG ACAAATTTTA       420
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Does Not Comply
Corrected Diskette Needed

See attached P. 7

RAW SEQUENCE LISTING   DATE: 10/07/2003
PATENT APPLICATION: US/10/675,226   TIME: 14:16:37

Input Set : A:\14233.10USU1-Romeo-Sequence Listing.txt
Output Set: N:\CRF4\10072003\J675226.raw

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 73 ACCCTGGCAG ATGCTGGTCA CTATGATACT GCGCTGGTTA AACTTAAGCA GCTTAACTCT    480
 75 GGAGCACCGG ACAAAGCCAA TTTACTCGCA GAAGCCTATA TCTATAAACT GGCGGGGCGT    540
 77 CATCAGGATG AATTACGGGC GATGACAGAG TCATTACCTG AAAATGCATC TACGCAACAA    600
 79 TATCCCACAG AATACGTGCA GGCATTACGT AATAATCAAC TTGCTGCCGC GATTGACGAT    660
 81 GCCAATTTAA CGCCAGATAT TCGCGCTGAT ATTCATGCCG AACTGGTCAG ACTGTCGTTT    720
 83 ATGCCTACGC GCAGTGAAAG TGAACGTTAT GCCATTGCCG ATCGCGCCCT CGCCCAATAC    780
 85 GCTGCATTAG AAATTCTGTG GCACGATAAC CCAGACCGCA CTGCCCAGTA CCAGCGTATT    840
 87 CAGGTTGATC ATCTTGGCGC GTTATTAACT CGCGATCGTT ATAAAGACGT TATTTCTCAC    900
 89 TATCAGCGAT TAAAAAAGAC GGGGCAAATT ATTCCGCCCT GGGGGCAATA TTGGGTTGCA    960
 91 TCGGCTTATC TCAAAGATCA TCAGCCGAAA AAAGCACAGT CAATAATGAC CGAGCTCTTT   1020
 93 TATCACAAGG AGACCATTGC CCCGGATTTA TCCGATGAAG AACTTGCGGA TCTCTTTTAC   1080
 95 AGCCACCTGG AGAGTGAAAA TTATCCGGGC GCGCTAACTG TCACCCAACA TACCATTAAT   1140
 97 ACTTCGCCGC CTTTCCTTCG GTTAATGGGC ACGCCTACGA GCATCCCGAA TGATACCTGG   1200
 99 TTACAGGGGC ATTCGTTTCT CTCAACCGTA GCAAAATATA GTAATGATCT TCCTCAGGCT   1260
101 GAAATGACAG CCAGAGAGCT TGCTTATAAC GCACCAGGAA ATCAGGGACT GCGCATTGAT   1320
103 TACGCGAGTG TGTTACAAGC CCGCGGTTGG CCTCGTGCAG CAGAAAATGA ATTAAAAAAA   1380
105 GCAGAAGTGA TCGAGCCACG TAATATTAAT CTGGAGGTTG AACAAGCCTG GACAGCATTA   1440
107 ACGTTACAAG AATGGCAGCA GGCAGCTGTC TTAACGCACG ATGTTGTCGA ACGTGAACCG   1500
109 CAAGATCCCG GCGTTGTACG ATTAAAACGT GCGGTTGATG TACATAATCT TGCAGAGCTT   1560
111 CGTATCGCTG GCTCAACAGG AATTGATGCC GAAGGCCCGG ATAGTGGTAA ACATGATGTC   1620
113 GACTTAACCA CCATCGTTTA TTCACCACCG CTGAAGGATA ACTGGCGCGG TTTTGCTGGA   1680
115 TTCGGTTATG CCGATGGACA ATTTAGCGAA GGAAAAGGGA TTGTTCGCGA CTGGCTTGCG   1740
117 GGTGTTGAGT GGCGGTCACG TAATATCTGG CTCGAGGCAG AGTACGCTGA ACGCGTTTTC   1800
119 AATCATGAGC ATAAACCCGG CGCGCGCCTG TCTGGCTGGT ATGATTTTAA TGATAACTGG   1860
121 CGTATTGGTT CGCAACTGGA ACGCCTCTCT CACCGCGTTC CATTACGGGC AATGAAAAAT   1920
123 GGTGTTACAG GCAACAGTGC TCAGGCTTAT GTTCGCTGGT ATCAAAATGA GCGGCGTAAG   1980
125 TACGGTGTCT CCTGGGCTTT CACTGATTTT TCCGACAGTA ACCAGCGTCA TGAAGTCTCA   2040
127 CTTGAGGGTC AGGAACGCAT CTGGTCTTCA CCATATTTGA TTGTCGATTT CCTACCCAGT   2100
129 CTGTATTACG AACAAAATAC AGAACACGAT ACCCCATACT ACAACCCTAT AAAAACGTTC   2160
131 GATATTGTTC CGGCATTTGA GGCAAGCCAT TTGTTATGGC GAAGCTATGA AAATAGCTGG   2220
133 GAGCAAATAT TCAGCGCAGG TGTTGGTGCC TCCTGGCAAA AACATTATGG CACGGATGTC   2280
135 GTCACCCAAC TCGGCTACGG GCAACGCATT AGTTGGAATG ACGTGATTGA TGCTGGCGCA   2340
137 ACGCTACGCT GGGAAAAACG ACCTTATGAC GGTGACAGAG AACACAACTT ATACGTTGAA   2400
139 TTCGATATGA CATTCAGATT TTAAGGATAA ATATGTTACG TAATGGAAAT AAATATCTCC   2460
142 (2)  INFORMATION FOR SEQ ID NO: 2:
144       (i)  SEQUENCE CHARACTERISTICS:
145            (A)  LENGTH: 807 amino acids
146            (B)  TYPE: amino acid
147            (C)  STRANDEDNESS: unknown
148            (D)  TOPOLOGY: unknown
150      (ii)  MOLECULE TYPE: peptide
152     (iii)  HYPOTHETICAL: NO
154      (iv)  ANTI-SENSE: NO
156      (vi)  ORIGINAL SOURCE:
157            (A)  ORGANISM: E. coli
160      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO: 2:
162       Met Tyr Ser Ser Ser Arg Lys Arg Cys Pro Lys Thr Lys Trp Ala Leu
163       1               5                  10                  15
165       Lys Leu Leu Thr Ala Ala Phe Leu Ala Ala Ser Pro Ala Ala Lys Ser
```

C--> at line 154

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166                  20                25                30
168      Ala Val Asn Asn Ala Tyr Asp Ala Leu Ile Ile Glu Ala Arg Lys Gly
169              35                40                45
171      Asn Thr Gln Pro Ala Leu Ser Trp Phe Ala Leu Lys Ser Ala Leu Ser
172          50                55                60
174      Asn Asn Gln Ile Ala Asp Trp Leu Gln Ile Ala Leu Trp Ala Gly Gln
175      65                70                75                80
177      Asp Lys Gln Val Ile Thr Val Tyr Asn Arg Tyr Arg His Gln Gln Leu
178              85                90                95
180      Pro Ala Arg Gly Tyr Ala Ala Val Ala Val Ala Tyr Arg Asn Leu Gln
181              100               105               110
183      Gln Trp Gln Asn Ser Leu Thr Leu Trp Gln Lys Ala Leu Ser Leu Glu
184          115               120               125
186      Pro Gln Asn Lys Asp Tyr Gln Arg Gly Gln Ile Leu Thr Leu Ala Asp
187          130               135               140
189      Ala Gly His Tyr Asp Thr Ala Leu Val Lys Leu Lys Gln Leu Asn Ser
190      145               150               155               160
192      Gly Ala Pro Asp Lys Ala Asn Leu Leu Ala Glu Ala Tyr Ile Tyr Lys
193              165               170               175
195      Leu Ala Gly Arg His Gln Asp Glu Leu Arg Ala Met Thr Glu Ser Leu
196              180               185               190
198      Pro Glu Asn Ala Ser Thr Gln Gln Tyr Pro Thr Glu Tyr Val Gln Ala
199          195               200               205
201      Leu Arg Asn Asn Gln Leu Ala Ala Ala Ile Asp Asp Ala Asn Leu Thr
202          210               215               220
204      Pro Asp Ile Arg Ala Asp Ile His Ala Glu Leu Val Arg Leu Ser Phe
205      225               230               235               240
207      Met Pro Thr Arg Ser Glu Ser Glu Arg Tyr Ala Ile Ala Asp Arg Ala
208              245               250               255
210      Leu Ala Gln Tyr Ala Ala Leu Glu Ile Leu Trp His Asp Asn Pro Asp
211              260               265               270
213      Arg Thr Ala Gln Tyr Gln Arg Ile Gln Val Asp His Leu Gly Ala Leu
214          275               280               285
216      Leu Thr Arg Asp Arg Tyr Lys Asp Val Ile Ser His Tyr Gln Arg Leu
217          290               295               300
219      Lys Lys Thr Gly Gln Ile Ile Pro Pro Trp Gly Gln Tyr Trp Val Ala
220      305               310               315               320
222      Ser Ala Tyr Leu Lys Asp His Gln Pro Lys Lys Ala Gln Ser Ile Met
223              325               330               335
225      Thr Glu Leu Phe Tyr His Lys Glu Thr Ile Ala Pro Asp Leu Ser Asp
226              340               345               350
228      Glu Glu Leu Ala Asp Leu Phe Tyr Ser His Leu Glu Ser Glu Asn Tyr
229              355               360               365
231      Pro Gly Ala Leu Thr Val Thr Gln His Thr Ile Asn Thr Ser Pro Pro
232          370               375               380
234      Phe Leu Arg Leu Met Gly Thr Pro Thr Ser Ile Pro Asn Asp Thr Trp
235      385               390               395               400
237      Leu Gln Gly His Ser Phe Leu Ser Thr Val Ala Lys Tyr Ser Asn Asp
238              405               410               415
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/675,226

DATE: 10/07/2003
TIME: 14:16:37

Input Set : A:\14233.10USU1-Romeo-Sequence Listing.txt
Output Set: N:\CRF4\10072003\J675226.raw

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240    Leu Pro Gln Ala Glu Met Thr Ala Arg Glu Leu Ala Tyr Asn Ala Pro
241                420                 425                 430
243    Gly Asn Gln Gly Leu Arg Ile Asp Tyr Ala Ser Val Leu Gln Ala Arg
244            435                 440                 445
246    Gly Trp Pro Arg Ala Ala Glu Asn Glu Leu Lys Lys Ala Glu Val Ile
247        450                 455                 460
249    Glu Pro Arg Asn Ile Asn Leu Glu Val Glu Gln Ala Trp Thr Ala Leu
250    465                 470                 475                 480
252    Thr Leu Gln Glu Trp Gln Gln Ala Ala Val Leu Thr His Asp Val Val
253                485                 490                 495
255    Glu Arg Glu Pro Gln Asp Pro Gly Val Val Arg Leu Lys Arg Ala Val
256            500                 505                 510
258    Asp Val His Asn Leu Ala Glu Leu Arg Ile Ala Gly Ser Thr Gly Ile
259            515                 520                 525
261    Asp Ala Glu Gly Pro Asp Ser Gly Lys His Asp Val Asp Leu Thr Thr
262        530                 535                 540
264    Ile Val Tyr Ser Pro Pro Leu Lys Asp Asn Trp Arg Gly Phe Ala Gly
265    545                 550                 555                 560
267    Phe Gly Tyr Ala Asp Gly Gln Phe Ser Glu Gly Lys Gly Ile Val Arg
268            565                 570                 575
270    Asp Trp Leu Ala Gly Val Glu Trp Arg Ser Arg Asn Ile Trp Leu Glu
271        580                 585                 590
273    Ala Glu Tyr Ala Glu Arg Val Phe Asn His Glu His Lys Pro Gly Ala
274        595                 600                 605    .
276    Arg Leu Ser Gly Trp Tyr Asp Phe Asn Asp Asn Trp Arg Ile Gly Ser
277        610                 615                 620
279    Gln Leu Glu Arg Leu Ser His Arg Val Pro Leu Arg Ala Met Lys Asn
280    625                 630                 635                 640
282    Gly Val Thr Gly Asn Ser Ala Gln Ala Tyr Val Arg Trp Tyr Gln Asn
283            645                 650                 655
285    Glu Arg Arg Lys Tyr Gly Val Ser Trp Ala Phe Thr Asp Phe Ser Asp
286            660                 665                 670
288    Ser Asn Gln Arg His Glu Val Ser Leu Glu Gly Gln Glu Arg Ile Trp
289            675                 680                 685
291    Ser Ser Pro Tyr Leu Ile Val Asp Phe Leu Pro Ser Leu Tyr Tyr Glu
292            690                 695                 700
294    Gln Asn Thr Glu His Asp Thr Pro Tyr Tyr Asn Pro Ile Lys Thr Phe
295    705                 710                 715                 720
297    Asp Ile Val Pro Ala Phe Glu Ala Ser His Leu Leu Trp Arg Ser Tyr
298                725                 730                 735
300    Glu Asn Ser Trp Glu Gln Ile Phe Ser Ala Gly Val Gly Ala Ser Trp
301            740                 745                 750
303    Gln Lys His Tyr Gly Thr Asp Val Val Thr Gln Leu Gly Tyr Gly Gln
304            755                 760                 765
306    Arg Ile Ser Trp Asn Asp Val Ile Asp Ala Gly Ala Thr Leu Arg Trp
307        770                 775                 780
309    Glu Lys Arg Pro Tyr Asp Gly Asp Arg Glu His Asn Leu Tyr Val Glu
310    785                 790                 795                 800
312    Phe Asp Met Thr Phe Arg Phe
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313                      805
315 (2) INFORMATION FOR SEQ ID NO: 3:
317       (i) SEQUENCE CHARACTERISTICS:
318           (A) LENGTH: 2031 base pairs
319           (B) TYPE: nucleic acid
320           (C) STRANDEDNESS: unknown
321           (D) TOPOLOGY: unknown
323      (ii) MOLECULE TYPE: DNA (genomic)
325     (iii) HYPOTHETICAL: NO
C--> 327    (iv) ANTI-SENSE: NO
329      (vi) ORIGINAL SOURCE:
330           (A) ORGANISM: E. coli
333      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
335 TTAAGGATAA ATATGTTACG TAATGGAAAT AAATATCTCC TGATGCTGGT GAGTATAATT      60
337 ATGCTCACCG CGTGCATTAG CCAGTCAAGA ACATCATTTA TACCGCCACA GGATCGCGAA     120
339 TCTTTACTCG CCGAGCAACC GTGGCCGCAT AATGGTTTTG TAGCGATTTC ATGGCATAAC     180
341 GTTGAAGACG AAGCTGCCGA CCAGCGTTTT ATGTCAGTGC GGACATCAGC ACTGCGTGAA     240
343 CAATTTGCCT GGCTGCGCGA GAACGGTTAT CAACCGGTCA GTATTGCTCA AATTCGTGAA     300
345 GCACATCGAG GAGGAAAACC GCTACCGGAA AAAGCTGTAG TGCTGACTTT TGATGACGGC     360
347 TACCAGAGTT TTTATACCCG CGTCTTCCCA ATTCTTCAGG CCTTCCAGTG GCCTGCTGTA     420
349 TGGGCCCCCG TCGGCAGTTG GGTCGATACG CCAGCGGATA AACAAGTAAA ATTTGGCGAT     480
351 GAGTTGGTCG ATCGAGAATA TTTTGCCACG TGGCAACAAG TGCGAGAAGT TGCGCGTTCC     540
353 CGGCTCGTTG AGCTCGCTTC TCATACATGG AATTCTCACT ACGGTATTCA GGCTAATGCC     600
355 ACCGGCAGCT TATTGCCTGT ATATGTAAAT CGTGCATATT TTACTGACCA CGCACGGTAT     660
357 GAAACCGCAG CAGAATACCG GGAAAGAATT CGTCTGGATG CTGTAAAAAT GACGGAATAC     720
359 CTGCGTACAA AGGTTGAGGT AAATCCACAC GTTTTTGTTT GGCCTTATGG CGAAGCGAAT     780
361 GGCATAGCGA TAGAGGAATT AAAAAAACTC GGTTATGACA TGTTCTTCAC CCTTGAATCA     840
363 GGTTTGGCAA ATGCGTCGCA ATTGGATTCC ATTCCGCGGG TATTAATCGC CAATAATCCC     900
365 TCATTAAAAG AGTTTGCCCA GCAAATTATT ACCGTACAGG AAAAATCACC ACAACGGATA     960
367 ATGCATATCG ATCTTGATTA CGTTTATGAC GAAAACCTCC AGCAAATGGA TCGCAATATT    1020
369 GATGTGCTAA TTCAGCGGGT GAAAGATATG CAAATATCAA CCGTGTATTT GCAGGCATTT    1080
371 GCTGATCCCG ATGGTGATGG GCTGGTCAAA GAGGTCTGGT TTCCAAATCG TTTGCTACCA    1140
373 ATGAAAGCAG ATATTTTTAG TCGGGTTGCC TGGCAATTAC GTACCCGCTC AGGTGTAAAC    1200
375 ATCTATGCGT GGATGCCGGT ATTAAGCTGG GATTTAGATC CCACATTAAC GCGAGTAAAA    1260
377 TACTTACCAA CAGGGGAGAA AAAAGCACAA ATTCATCCTG AACAATATCA CCGTCTCTCT    1320
379 CCTTTCGATG ACAGAGTCAG AGCACAAGTT GGCATGTTAT ATGAAGATCT TGCCGGACAT    1380
381 GCTGCTTTTG ATGGCATATT GTTCCACGAT GATGCTTTGC TTTCAGATTA TGAAGATGCC    1440
383 AGTGCACCGG CTATCACGGC TTATCAGCAA GCAGGCTTTA GCGGGAGTCT GAGCGAAATT    1500
385 CGACAAAACC CGGAGCAATT TAAACAGTGG GCCCGCTTTA AAAGTCGTGC GTTAACTGAC    1560
387 TTCACTTTAG AACTTAGTGC GCGCGTAAAA GCCATTCGCG TCCACATAT TAAAACTGCA    1620
389 CGAAATATTT TTGCACTTCC GGTAATACAA CCTGAAAGTG AAGCCTGGTT TGCACAGAAT    1680
391 TATGCTGATT TCCTAAAAAG CTATGACTGG ACCGCTATTA TGGCTATGCC TTATCTGGAA    1740
393 GGTGTCGCAG AAAAATCGGC TGACCAATGG TTAATACAAT TGACCAATCA AATTAAAAAC    1800
395 ATCCCTCAGG CTAAAGACAA ATCTATTTTA GAATTACAGG CACAAAACTG GCAGAAAAAT    1860
397 GGTCAGCATC AGGCTATTTC TTCGCAACAA CTCGCTCACT GGATGAGCCT ATTACAACTG    1920
399 AATGGAGTGA AAAACTATGG TTATTATCCC GACAATTTTC TGCATAACCA ACCTGAAATA    1980
401 GACCTTATTC GTCCTGAGTT TTCAACAGCC TGGTATCCGA AAAATGATTA A            2031
403 (2) INFORMATION FOR SEQ ID NO: 4:
405       (i) SEQUENCE CHARACTERISTICS:
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VERIFICATION SUMMARY
PATENT APPLICATION: **US/10/675,226**

DATE: 10/07/2003
TIME: 14:16:38

Input Set : **A:\14233.10USU1-Romeo-Sequence Listing.txt**
Output Set: **N:\CRF4\10072003\J675226.raw**

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L:7 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:] of (1) line corrected
L:8 M:238 W: Alpha Fields not Ordered, Reordered [(B) STREET:] of (1)(iv)
L:12 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:13 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:14 M:220 C: Keyword misspelled or invalid format, [(B) TELEFAX:]
L:16 M:238 W: Alpha Fields not Ordered, Reordered [(A) NAME:] of (1)(viii)
L:17 M:238 W: Alpha Fields not Ordered, Reordered [(B) STREET:] of (1)(iv)
L:21 M:220 C: Keyword misspelled or invalid format, [(F) ZIP:]
L:22 M:220 C: Keyword misspelled or invalid format, [(A) TELEPHONE:]
L:23 M:220 C: Keyword misspelled or invalid format, [(B) TELEFAX:]
L:25 M:238 W: Alpha Fields not Ordered, Reordered [(ii) TITLE OF INVENTION:] of (1)
L:30 M:220 C: Keyword misspelled or invalid format, [(v) COMPUTER READABLE FORM:]
L:36 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:36 M:220 C: Keyword misspelled or invalid format, [(vi) CURRENT APPLICATION DATA:]
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:37 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:0 M:247 C: Inserted Optional Header Field, [(viii) ATTORNEY/AGENT INFORMATION:]
L:0 M:247 C: Inserted Optional Header Field, [(ix) TELECOMMUNICATION INFORMATION:]
L:0 M:249 C: Inserted Mandatory Field, [(B) FILING DATE:]
L:51 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:154 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:327 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:415 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:562 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:629 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:733 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:755 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
L:777 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: *↑ move to (i) APPLICANT line*

~~(A) NAME:~~ Romeo, Tony
~~(B) STREET: c/o Ridout & Maybee~~
~~(C) CITY: Toronto~~
~~(D) STATE: Ont~~
~~(E) COUNTRY: Canada~~
~~(F) POSTAL CODE (ZIP): M5C 3B1~~
~~(G) TELEPHONE: 4168653505~~
~~(H) TELEFAX: 4163620823~~

delete

~~(A)~~ NAME: Wang, Xin *move under first applicant*
~~(B) STREET: c/o Ridout & Maybee~~
~~(C) CITY: Toronto~~
~~(D) STATE: Ont~~
~~(E) COUNTRY: Canada~~
~~(F) POSTAL CODE (ZIP): M5C 3B1~~
~~(G) TELEPHONE: 4168653505~~
~~(H) TELEFAX: 4163621482~~

delete

(ii) TITLE OF INVENTION: Methods for Polysaccharide Adhesin Synthesis
     Modulation

(iii) NUMBER OF SEQUENCES: 9

(V) ~~(iv)~~ COMPUTER READABLE FORM:
    (A) MEDIUM TYPE: Floppy disk
    (B) COMPUTER: IBM PC compatible
    (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    (D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) CORRESPONDENCE ADDRESS:
    (A) ADDRESSEE:
    (B) STREET:
    (C) CITY:
    (D) STATE:
    (E) COUNTRY:
    (F) ZIP:

insert these MANDATORY headings and then responses for a U.S. application

(vi) ~~(v)~~ CURRENT APPLICATION DATA:
insert → (A) APPLICATION NUMBER: (CA 2,411,508) *this is not the current application number*
insert → (B) FILING DATE:

insert → (vii) PRIOR APPLICATION DATA:
    (A) APPLICATION NUMBER:
    (B) FILING DATE: *mandatory response*

insert these MANDATORY headings and responses

EPO format is invalid for a U.S. application